

SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: VETIGEN  
 (B) STREET: 21 rue Sébastien Mercier  
 (C) CITY: PARIS  
 (E) COUNTRY: FRANCE  
 (F) POSTAL CODE (ZIP): 75015

(A) NAME: LENZEN Gerlinde  
 (B) STREET: 55 rue des Cévennes  
 (C) CITY: PARIS  
 (E) COUNTRY: FRANCE  
 (F) POSTAL CODE (ZIP): 75015

(A) NAME: STROSBERG Arthur Donny  
 (B) STREET: 66 rue de Javel  
 (C) CITY: PARIS  
 (E) COUNTRY: FRANCE  
 (F) POSTAL CODE (ZIP): 75015

(A) NAME: SUGASAWA Toshinari  
 (B) STREET: 9-12-507 Miyano-cho, Takatsuki-shi  
 (C) CITY: OSAKA  
 (E) COUNTRY: JAPON  
 (F) POSTAL CODE (ZIP): 569

(A) NAME: MOROOKA Shigeako  
 (B) STREET: 4-78 nishi-3, Seiwadai, Kawanishi-shi  
 (C) CITY: HYOGO  
 (E) COUNTRY: JAPON  
 (F) POSTAL CODE (ZIP): 666-01

(ii) TITLE OF INVENTION: NON-ADRENERGIC RECEPTOR AND ITS APPLICATIONS.

(iii) NUMBER OF SEQUENCES: 14

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met	Tyr	Ile	Asp	Asp	Leu	Pro	Ile	Trp	Gly	Ile	Val	Gly	Glu	Ala	Asp
1					5				10					15	
Glu	Asn	Gly	Glu	Asp	Tyr	Tyr	Leu	Trp	Thr	Tyr	Lys	Lys	Leu	Glu	Ile
		20					25						30		
Gly	Phe	Asn	Gly	Asn	Arg	Ile	Val	Asp	Val	Asn	Leu	Thr	Ser	Glu	Gly
	35					40						45			

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Lys Val Lys Leu Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val  
 50 55 60  
 Lys Trp Lys Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr  
 65 70 75 80  
 Leu Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe  
 85 90 95  
 Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile  
 100 105 110  
 Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu  
 115 120 125  
 Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys  
 130 135 140  
 Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe  
 145 150 155 160  
 Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile  
 165 170 175  
 Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser  
 180 185 190  
 Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn  
 195 200 205  
 Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp  
 210 215 220  
 Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys  
 225 230 235 240  
 Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser  
 245 250 255  
 Arg Ala Ile Pro Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe  
 260 265 270  
 Phe Val Ile Leu Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn  
 275 280 285  
 Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg  
 290 295 300  
 Pro Ile Pro Glu Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys  
 305 310 315 320  
 Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe  
 325 330 335  
 Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe  
 340 345 350  
 Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr  
 355 360 365  
 Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln  
 370 375 380  
 Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met  
 385 390 395 400  
 Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe  
 405 410 415

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 668060-4267660

Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu  
 420 425 430

Gly Ile Met Cys Gly Ala Ile  
 435

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGTACATAG ATGATTTACC AATATGGGGT ATTGTTGGTG AGGCTGATGA AAATGGAGAA 60  
 GATTACTATC TTTGGACCTA TAAAAAAGTT GAAATAGGTT TTAATGGAAA TCGAATTGTT 120  
 GATGTTAATC TAACTAGTGA AGGAAAGGTG AACTGGTTC CAAATACTAA AATCCAGATG 180  
 TCATATTCAG TAAATGGAA AAAGTCAGAT GTGAAATTG AAGATCGATT TGACAAATAT 240  
 CTTGATCCGT CCTTTTTTCA ACATCGGATT CATTGGTTTT CAATTTTCAA CTCCTTCATG 300  
 ATGGTGATCT TCTTGGTGGG CTTAGTTTCA ATGATTTTAA TGAGAACATT AAGAAAAGAT 360  
 TATGCTCGGT ACAGTAAAGA GGAAGAAATG GATGATATGG ATAGAGACCT AGGAGATGAA 420  
 TATGGATGGA AACAGGTGCA TGGAGATGTA TTAGACCAT CAAGTCACCC ACTGATATTT 480  
 TCCTCTCTGA TTGGTTCTGG ATGTCAGATA TTGCTGTGT CTCTCATCGT TATTATTGTT 540  
 GCAATGATAG AAGATTTATA TACTGAGAGG GGATCAATGC TCAGTACAGC CATATTTGTC 600  
 TATGCTGCTA CGTCTCCAGT GAATGGTTAT TTTGGAGGAA GTCTGTATGC TAGACAAGGA 660  
 GGAAGGAGAT GGATAAAGCA GATGTTTATT GGGGCATTCC TTATCCCAGC TATGGTGTGT 720  
 GGCACCTGCCT TCTTCATCAA TTTCATAGCC ATTTATTACC ATGCTTCAAG AGCCATTCCT 780  
 TTTGGAACAA TGGTGGCCGT TTGTTGCATC TGTTTTTTTG TTATTCTTCC TCTAAATCTT 840  
 GTTGGTACAA TACTTGGCCG AAATCTGTCA GGTGAGCCCA ACTTTCCTTG TCGTGTCAAT 900  
 GCTGTGCCTC GTCCTATACC GGAGAAAAAA TGGTTCATGG AGCCTGCGGT TATTGTTTGC 960  
 CTGGGTGGAA TTTTACCTTT TGGTTCAATC TTTATTGAAA TGTATTTTCA CTTCACGTCT 1020  
 TTCTGGGCAT ATAAGATCTA TTATGTCTAT GGCTTCATGA TGCTGGTGCT GGTATCCTG 1080  
 TGCATTGTGA CTGTCTGTGT GACTATTGTG TGCACATATT TTCTACTAAA TGCAGAAGAT 1140  
 TACCGGTGGC AATGGACAAG TTTTCTCTCT GCTGCATCAA CTGCAATCTA TGTTTACATG 1200  
 TATTCTTTT ACTACTATTT TTCAAACA AAGATGTATG GCTTATTTCA AACATCATTT 1260  
 TACTTTGGAT ATATGGCGGT ATTTAGCACA GCCTTGGGGA TAATGTGTGG AGCGATT 1317

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## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 965 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGATGTCAT ATTCAGTAA ATGGAAG TCAGATGTGA AATTTGAAGA TCGATTTGAC 60  
AAATATCTTG ATCCGTCCTT TTTTCAACAT CGGATTCATT GGTTTTCAAT TTTCAACTCC 120  
TTCATGATGG TGATCTTCTT GGTGGGCTTA GTTTCAATGA TTTTAATGAG AACATTAAGA 180  
AAAGATTATG CTCGGTACAG TAAAGAGGAA GAAATGGATG ATATGGATAG AGACCTAGGA 240  
GATGAATATG GATGGAACA GGTGCATGGA GATGTATTTA GACCATCAAG TCACCCACTG 300  
ATATTTTCTT CTCTGATTGG TTCTGGATGT CAGATATTTG CTGTGTCTCT CATCGTTATT 360  
ATTGTTGCAA TGATAGAAGA TTTATATACT GAGAGGGGAT CAATGCTCAG TACAGCCATA 420  
TTTGTCTATG CTGCTACGTC TCCAGTGAAT GGTTATTTTA GAGGAAGTCT GTATGCTAGA 480  
CAAGGAGGAA GGAGATGGAT AAAGCAGATG TTTATTGGGG CATTCCTTAT CCCAGCTATG 540  
GTGTGTGGCA CTGCCTTCTT CATCAATTTT ATAGCCATTT ATTACCATGC TTCAAGAGCC 600  
ATTCCTTTTG GAACAATGGT GGCCGTTTGT TGCATCTGTT TTTTGTAT TCTTCCTCTA 660  
AATCTTGTG GTACAATACT TGGCCGAAAT CTGTCAGGTC AGCCCAACTT TCCTTGTCGT 720  
GTCAATGCTG TGCCTCGTCC TATACCGGAG AAAAAATGGT TCATGGAGCC TGCGGTTATT 780  
GTTGCCTGG GTGGAATTTT ACCTTTTGGT TCAATCTTTA TTGAAATGTA TTTTCATCTT 840  
ACGTCTTTCT GGGCATATAA GATCTATTAT GTCTATGCT TCATGATGCT GGTGCTGGTT 900  
ATCCTGTGCA TTGTGACTGT CTGTGTGACT ATTGTGTGCA CATATTTTCT ACTAAATGCA 960  
GAAGA 965

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCAGTAAAAT GGAAAAAGTC AGATGTGAAA TTTGAAGATC GATTGACAA ATATCTTGAT 60  
CCGTCCTTTT TTCAACATCG GATTCATTGG TTTTCAATTT TCAACTCCTT CATGATGGTG 120  
ATCTTCTTGG TGGGCTTAGT TTCAATGATT TTAATGAGAA CATTAGAAA AGATTATGCT 180  
CGGTACAGTA AAGAGGAAGA AATGGATGAT ATGGATAGAG ACCTAGGAGA TGAATATGGA 240  
TGGAAACAGG TGCATGGAGA TGTATTTAGA CCATCAAGTC ACCCA 285

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## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe Asn  
 1                      5                      10                      15  
 Ser

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp Pro Xaa Phe Phe Gln His Arg Ile His Val Phe Ser Ile Phe Asn  
 1                      5                      10                      15  
 His

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "AMORCE"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCAGTAAAAT GGAAAAAGTC

20

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "AMORCE"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TGGGTGACTT GATGGTCTAA

20

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "AMORCE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCTGTGTCTC TCATCGTTA

19

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "AMORCE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CCATCCATAT TCATCTCCTA

20

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "AMORCE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGGTATAGGA CGAGGCACAG C

21

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "AMORCE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ACTGAATATG ACATCTGG

18

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## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1800 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 3..1730

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CC GCC GCG CTG TGG CTG CTG CTG CTG CTG CCC CGG ACC CGG GCG 47  
 Ala Ala Leu Trp Leu Leu Leu Leu Leu Pro Arg Thr Arg Ala  
 1 5 10 15

GAC GAG CAC GAA CAC ACG TAT CAA GAT AAA GAG GAA GTT GTC TTA TGG 95  
 Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp  
 20 25 30

ATG AAT ACT GTT GGG CCC TAC CAT AAT CGT CAA GAA ACA TAT AAG TAC 143  
 Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr  
 35 40 45

TTT TCA CTT CCA TTC TGT CTG GGG TCA AAA AAA AGT ATC AGT CAT TAC 191  
 Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr  
 50 55 60

CAT GAA ACT CTG GGA GAA GCA CTT CAA GGG GTT GAA TTG GAA TTT AGT 239  
 His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser  
 65 70 75

GGT CTG GAT ATT AAA TTT AAA GAT GAT GTG ATG CCA GCC ACT TAC TGT 287  
 Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys  
 80 85 90 95

GAA ATT GAT TTA GAT AAA GAA AAG AGA GAT GCA TTT GTA TAT GCC ATA 335  
 Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile  
 100 105 110

AAA AAT CAT TAC TGG TAC CAG ATG TAC ATA GAT GAT TTA CCA ATA TGG 383  
 Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp  
 115 120 125

GGT ATT GTT GGT GAG GCT GAT GAA AAT GGA GAA GAT TAC TAT CTT TGG 431  
 Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp  
 130 135 140

ACC TAT AAA AAA CTT GAA ATA GGT TTT AAT GGA AAT CGA ATT GTT GAT 479  
 Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp  
 145 150 155

GTT AAT CTA ACT AGT GAA GGA AAG GTG AAA CTG GTT CCA AAT ACT AAA 527  
 Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys  
 160 165 170 175

ATC CAG ATG TCA TAT TCA GTA AAA TGG AAA AAG TCA GAT GTG AAA TTT 575  
 Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe  
 180 185 190

GAA GAT CGA TTT GAC AAA TAT CTT GAT CCG TCC TTT TTT CAA CAT CGG 623  
 Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg  
 195 200 205

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ATT CAT TGG TTT TCA ATT TTC AAC TCC TTC ATG ATG GTG ATC TTC TTG 671  
 Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu  
 210 215 220

GTG GGC TTA GTT TCA ATG ATT TTA ATG AGA ACA TTA AGA AAA GAT TAT 719  
 Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr  
 225 230 235

GCT CGG TAC AGT AAA GAG GAA GAA ATG GAT GAT ATG GAT AGA GAC CTA 767  
 Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu  
 240 245 250 255

GGA GAT GAA TAT GGA TGG AAA CAG GTG CAT GGA GAT GTA TTT AGA CCA 815  
 Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro  
 260 265 270

TCA AGT CAC CCA CTG ATA TTT TCC TCT CTG ATT GGT TCT GGA TGT CAG 863  
 Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln  
 275 280 285

ATA TTT GCT GTG TCT CTC ATC GTT ATT ATT GTT GCA ATG ATA GAA GAT 911  
 Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp  
 290 295 300

TTA TAT ACT GAG AGG GGA TCA ATG CTC AGT ACA GCC ATA TTT GTC TAT 959  
 Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr  
 305 310 315

GCT GCT ACG TCT CCA GTG AAT GGT TAT TTT GGA GGA AGT CTG TAT GCT 1007  
 Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala  
 320 325 330 335

AGA CAA GGA GGA AGG AGA TGG ATA AAG CAG ATG TTT ATT GGG GCA TTC 1055  
 Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe  
 340 345 350

CTT ATC CCA GCT ATG GTG TGT GGC ACT GCC TTC TTC ATC AAT TTC ATA 1103  
 Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile  
 355 360 365

GCC ATT TAT TAC CAT GCT TCA AGA GCC ATT CCT TTT GGA ACA ATG GTG 1151  
 Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val  
 370 375 380

GCC GTT TGT TGC ATC TGT TTT TTT GTT ATT CTT CCT CTA AAT CTT GTT 1199  
 Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val  
 385 390 395

GGT ACA ATA CTT GGC CGA AAT CTG TCA GGT CAG CCC AAC TTT CCT TGT 1247  
 Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys  
 400 405 410 415

CGT GTC AAT GCT GTG CCT CGT CCT ATA CCG GAG AAA AAA TGG TTC ATG 1295  
 Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met  
 420 425 430

GAG CCT GCG GTT ATT GTT TGC CTG GGT GGA ATT TTA CCT TTT GGT TCA 1343  
 Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser  
 435 440 445

ATC TTT ATT GAA ATG TAT TTC ATC TTC ACG TCT TTC TGG GCA TAT AAG 1391  
 Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys  
 450 455 460

ATC TAT TAT GTC TAT GGC TTC ATG ATG CTG GTG CTG GTT ATC CTG TGC 1439  
 Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys  
 465 470 475

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ATT GTG ACT GTC TGT GTG ACT ATT GTG TGC ACA TAT TTT CTA CTA AAT 1487  
 Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn  
 480 485 490 495

GCA GAA GAT TAC CGG TGG CAA TGG ACA AGT TTT CTC TCT GCT GCA TCA 1535  
 Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser  
 500 505 510

ACT GCA ATC TAT GTT TAC ATG TAT TCC TTT TAC TAC TAT TTT TTC AAA 1583  
 Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys  
 515 520 525

ACA AAG ATG TAT GGC TTA TTT CAA ACA TCA TTT TAC TTT GGA TAT ATG 1631  
 Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met  
 530 535 540

GCG GTA TTT AGC ACA GCC TTG GGG ATA ATG TGT GGA GCG ATT GGT TAC 1679  
 Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr  
 545 550 555

ATG GGA ACA AGT GCC TTT GTC CGA AAA ATC TAT ACT AAT GTG AAA ATT 1727  
 Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile  
 560 565 570 575

GAC TAGAGACCCA AGAAAACCTG GAACTTTGGA TCAATTTCTT TTTCATAGGG 1780  
 Asp

GTGGAACTTG CACAGCAAAA 1800

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Ala Ala Leu Trp Leu Leu Leu Leu Leu Pro Arg Thr Arg Ala Asp  
 1 5 10 15  
 Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp Met  
 20 25 30  
 Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr Phe  
 35 40 45  
 Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr His  
 50 55 60  
 Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser Gly  
 65 70 75 80  
 Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys Glu  
 85 90 95  
 Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile Lys  
 100 105 110  
 Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly  
 115 120 125  
 Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr  
 130 135 140  
 Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp Val

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145 150 155 160  
 Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys Ile  
 165 170 175  
 Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe Glu  
 180 185 190  
 Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg Ile  
 195 200 205  
 His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu Val  
 210 215 220  
 Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala  
 225 230 235 240  
 Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu Gly  
 245 250 255  
 Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro Ser  
 260 265 270  
 Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile  
 275 280 285  
 Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp Leu  
 290 295 300  
 Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr Ala  
 305 310 315 320  
 Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg  
 325 330 335  
 Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe Leu  
 340 345 350  
 Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala  
 355 360 365  
 Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val Ala  
 370 375 380  
 Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val Gly  
 385 390 395 400  
 Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg  
 405 410 415  
 Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met Glu  
 420 425 430  
 Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile  
 435 440 445  
 Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile  
 450 455 460  
 Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile  
 465 470 475 480  
 Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala  
 485 490 495  
 Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr  
 500 505 510  
 Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr

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Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala  
530 535 540

Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr Met  
545 550 555 560

Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp  
565 570 575

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